

GenCore version 5.1.5  
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2003, 20:03:50 ; Search time 2844 Seconds  
(without alignments)  
12710.382 Million cell updates/sec

Title: US-09-625-573-1  
Perfect score: 2232  
Sequence: 1 GGATTGAACAGGACGCATT.....TATAACTATGTTGATAAAG 2232

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estim:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pin:\*  
21: em\_gss\_vit:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
c 1	396	17.7	457	9 AA694175	AA694175 z142a04.s
c 2	367	16.4	407	14 BQ027284	BQ027284 UI-H-CO0-
c 3	359	16.1	469	10 AV715904	AV715904 AV715904
c 4	352	15.8	398	9 AA807940	AA807940 nu90f10.s
c 5	272	12.2	563	9 AA034153	AA034153 z106f10.r
c 6	243	10.9	410	14 H58584	H58584 yr06f06.r1

AA034154	z106f10.s	289	10.7	238	7	8
H58597	yr06f06.r1	422	10.6	236	8	
H58254	yr06f06.s1	467	10.6	232	9	
H58245	yr06f06.s1	461	8.0	179	10	
B84215	RPC111-22K6	469	5.7	128	11	
AI312331	ta78e11.x	176	5.5	122	12	
BG315432	PO2.0.308	207	4.8	108	13	
BF175316	MYE4866.M	121	3.0	68	14	
BF1764263	603045953	807	2.9	65	15	
AA671573	vi04901.r	447	1.5	33	16	
BG56336	UI-M-BH0-	487	1.5	33	17	
AA547303		542	1.5	33	18	
AI851510	UI-M-BH0-	452	1.0	23	19	
BG292833	602389845	1236	1.0	22	20	
AA318949	EST21122	172	0.9	21	21	
BG940587	ax06e06.y	180	0.9	21	22	
BB386318	BB386318	296	0.9	21	23	
R53318	YQ82H04.r1	300	0.9	21	24	
BG09618	601501611	309	0.9	21	25	
H20897	Ym48f07.r1	310	0.9	21	26	
R25491	Yg44b06.r1	406	0.9	21	27	
AA281342	ZS94G08.r	410	0.9	21	28	
AI218647	Qf48C07.x	433	0.9	21	29	
AZ938335	ZM0196D24	445	0.9	21	30	
BM150403	TCBAP1D07	453	0.9	21	31	
AA436287	ZV22C03.r	472	0.9	21	32	
BE954472	UI-M-CEI-	525	0.9	21	33	
AA714861	nx93h11.s	555	0.9	21	34	
BH281895	CH230-191	610	0.9	21	35	
BF130511	601818643	632	0.9	21	36	
AZ417081	LM0192A12	633	0.9	21	37	
AW960725	EST372796	650	0.9	21	38	
BB630138	BB630138	670	0.9	21	39	
BQ787658	lm14b01.x	673	0.9	21	40	
BE883230	601508658	682	0.9	21	41	
AU127682	AU127682	778	0.9	21	42	
AU140261	AU140261	803	0.9	21	43	
BG104799	602311755	803	0.9	21	44	
AZ713219	RPCI-24-1				45	

#### ALIGNMENTS

RESULT 1  
AA694175/c  
LOCUS  
DEFINITION  
z142a04.s1 Soares\_fetal\_liver\_spleen\_LNFLS\_S1 Homo sapiens cDNA  
Clone IMAGE:433422 3', mRNA sequence.  
457 bp mRNA linear EST 16-DEC-1997  
AA694175  
AA694175.1 GI:2695113  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 457)  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin  
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,  
White, Y., Wyllie, T., Waterston, R. and Wilson, R.  
WashU-NCI human EST Project  
Unpublished (1997)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 455.





Query Match 10.9%; Score 243; DB 14; Length 410;





```

source
1. .461
/organism="Homo sapiens"
/db_xref="GDB:3773646"
/db_xref="taxon:9606"
/clone="IMAGE:204515"
/clone.lib="Soares fetal liver spleen lNFLS"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)
with a modified polylinker; Site_1: Pac I - oligo(dT) primer;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
[5', AACTGGAAGAATAAATTAAGATCTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."
119 a 97 c 96 g 144 t 5 others
BASE COUNT
ORIGIN

Query Match      8.0%; Score 179; DB 14; Length 461;
Best Local Similarity 99.6%; Pred.No. 3.6e-84;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 200 CCAGGCAACTGGGAAGTACCTCCCAAGCTGGACATATGCTCTACTTTTCAGGCCCATG 2059
Ddb 230 CCAGGCAACTGGGAAGTACCTCCCAAGCTGGACATATGCTCTACTTTTCAGGCCCATG 171
QY 2060 GCTAAAGAAGGTTTCAGAAGAAGTGGGCAGCAGACAGAACTTCACCTTCATATATTG 2119
Ddb 170 GCTAAAGAAGGTTTCAGAAGAAGTGGGCAGCAGACAGAACTTCACCTTCATATATTG 111
QY 2120 TATGATCCTTAATCAATGCATAAATGTTAAGTTTGATGGTATGAAATGTAATACTGTT 2179
Ddb 110 TATGATCCTTAATCAATGCATAAATGTTAAGTTTGATGGTATGAAATGTAATACTGTT 51
QY 2180 TTAAACAACATGATGTTTGGAAAATAAATCAATGCTATTAACATATGTTGTATA 2229
Ddb 50 TTAAACAACATGATGTTTGGAAAATAAATCAATGCTATTAACATATGTTGTATA 1

RESULT 11
B84215
LOCUS
DEFINITION
B84215
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

```

B84215  
RPCI11-22K6.TV RPCI-11 Homo sapiens genomic clone RPCI-11-22K6, DNA  
Sequence.  
B84215 GI:2925347  
GSS.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 469)  
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,  
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and  
Venet,J.C.  
Use of BAC End Sequences for Sequence-Ready Map Building (1998)  
Unpublished (1998)  
Other\_GSSs: RPCI11-22K6.TP  
Contact: Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: mdadams@tigr.org  
Clones are derived from the human BAC library Rpci-11. For BAC  
library availability, please contact Pieter de Jong  
(pieterdejong.med.buffalo.edu). Clones may be purchased from  
BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from  
Research Genetics ([inforesgen.com](http://inforesgen.com)). BAC end search page:



bone marrow, stem cells 34+/38+, cDNA made by oligo-dT priming. Directionally cloned. Size-selected on agarose gel, average insert size 400 bp. Primary library, non-amplified.

BASE COUNT 82 a 23 c 27 g 44 t

Query Match 5.5%; Score 122; DB 9; Length 176;  
Best Local Similarity 100.0%; Pred. No. 1.2e-53;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1290 GGTTGGAAACACTATTTCACAACTACCTCCAGTTCCTCATTTTGAATACAGGCAT 1349  
|||||  
Db 16 GGGTGGAAACACTATTTCACAACTACCTCCAGTTCCTCATTTTGAATACAGGCAT 75

QY 1350 AGAGTTCAGACTTTTAAATAGTAAATAAATAAAGCTGAAAGCTGCAACTTGTGA 1409  
|||||  
Db 76 AGAGTTCAGACTTTTAAATAGTAAATAAATAAAGCTGAAAGCTGCAACTTGTGA 135

QY 1410 AA 1411  
||  
Db 136 AA 137

RESULT 13  
BG315432  
LOCUS 207 bp mRNA linear EST 28-FEB-2002  
DEFINITION PO2.0.308 Human THP1 cell line library Homo sapiens cDNA, mRNA  
sequence.  
ACCESSION BG315432  
VERSION BG315432.1 GI:18998304  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Andersson,T., Borang,S., Larsson,M., Thelin,A., Ekstrand-Hammarstrom  
B., Wirta,V., Wenborg,A., Lundberg,J. and Odeberg,J.  
TITLE Identification of candidate genes in atherosclerosis - Virtual chip  
analysis in RDA based transcript profiling of monocyte/macrophage  
response to oxidised LDL  
JOURNAL Unpublished (2001)  
COMMENT Contact: Andersson Tove  
Department of Biotechnology  
KTH  
Teknikringen 34, plan 6, 100 44 Stockholm, Sweden  
Tel: +46 8 790 71 29  
Fax: +46 8 245452  
Email: tove@biochem.kth.se  
POLYA-No.

FEATURES Location/Qualifiers  
1..207  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="Human THP1 cell line library"  
/cell\_line="THP1"  
/note="Vector: pRIT28; Site\_1: BamHI; Site\_2: BamHI;  
Shotgun cloning of RDA difference products. Macrophage and  
foamcell libraries were submitted to successive rounds of  
subtractive hybridisations generating populations of gene  
fragments that are differentially expressed in macrophage  
to foam cell formation."

BASE COUNT 52 a 45 c 52 g 55 t 3 others

Query Match 4.8%; Score 108; DB 12; Length 207;  
Best Local Similarity 100.0%; Pred. No. 3.8e-46;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1244 GTCTAGTTACCGGAGGAGGCTGAGAGGAGAGACTCCAGCTGGGTGGAAACAG 1303  
|||||  
Db 100 GTCTAGTTACCGGAGGAGGCTGAGAGGAGAGACTCCAGCTGGGTGGAAACAG 159

QY 1304 TATTTCCAAACTACCTCCAGTTCCTCATTTTGAATACAGGCATAG 1351  
|||||  
Db 160 TATTTCCAAACTACCTCCAGTTCCTCATTTTGAATACAGGCATAG 207

RESULT 14  
BF175316  
LOCUS 121 bp mRNA linear EST 23-MAR-2001  
DEFINITION MYE4866 Myeloma (MYE) cDNA library Homo sapiens cDNA, mRNA  
sequence.  
ACCESSION BF175316  
VERSION BF175316.1 GI:13441530  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Claudio,J.O., Tang,H., Khan,E.M., Voralia,M., Li,Z., Cukerman,E.,  
Franciso-Pabalan,O., Liew,C.C. and Stewart,A.K.  
TITLE The transcriptional phenotype of myeloma cells  
JOURNAL Unpublished (2000)  
COMMENT Contact: A. Keith Stewart, M.D.  
Oncology Research  
University Health Network  
610 University Ave., 5-126, Toronto, Ontario, M5G 2M9, Canada  
Tel: (416) 946-4639  
Fax: (416) 946-6546  
Email: k.stewart@utoronto.ca  
PCR Primers  
FORWARD: 5'-GCCAGCTCGAATTAAACCTCACTAAAGGG-3'  
BACKWARD: 5'-CCAGTGAATTGTAATACGACTACTATAGGCG-3'  
Seq primer: 5'-GAATTAACCTCACTAAAGG-3'

FEATURES Location/Qualifiers  
1..121  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="Myeloma (MYE) cDNA library"  
/sex="male"  
/tissue\_type="Blood"  
/cell\_type="myeloma"  
/dev\_stage="multiple myeloma"  
/note="Vector: Lambda Zap Express; Site\_1: EcoRI; Site\_2:  
XhoI; Myeloma cells from multiple myeloma patients' bone  
marrow were purified by magnetic cell sorting. mRNA were  
purified and an oligo d(T)18 primer containing XhoI  
restriction site was used to prime first strand synthesis  
using M-MLV reverse transcriptase. To protect the cDNAs  
from XhoI digestion in subsequent cloning step, the  
nucleotide analogue 5-methyl-dCTP was added to the  
nucleotide mixture and [a-32P]dATP was added to monitor  
the quantity and quality of first strand synthesis. After  
second-strand synthesis and blunting of cDNA termini,  
EcoRI adapters were ligated, followed by kinase treatment  
and digestion with XhoI. The cDNAs were then  
size-fractionated using Sephacryl S-500 column and then  
ligated into EcoRI and XhoI digested Lambda Zap Express  
vector. The ligation product was packaged using Gigapack  
II packaging extract. The library had primary titre of  
approx. 1x10<sup>6</sup>. Clones from the primary library were  
randomly selected for single pass sequencing."

BASE COUNT 21 a 27 c 26 g 47 t

Query Match 3.0%; Score 68; DB 12; Length 121;  
Best Local Similarity 100.0%; Pred. No. 1e-24;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1674 CTCCTATCTCTCAGGCTTCTGCTGCAAAAGCCTTTTGTGTTTGTATCATTAAGAA 1733  
|||||  
Db 2 CTCCTATCTCTCAGGCTTCTGCTGCAAAAGCCTTTTGTGTTTGTATCATTAAGAA 61



Mon Jun '2 09:42:06 2003

QY 1734 GTCATGCG 1741  
|||||  
Db 62 GTCATGCG 69

RESULT 15  
BI764263 807 bp mRNA linear EST 25-SEP-2001  
LOCUS 603045953f1 NIH\_MGC\_116 Homo sapiens cDNA clone IMAGE:5186388 5',  
DEFINITION mRNA sequence.  
ACCESSION BI764263  
VERSION BI764263.1 GI:15755841  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 807)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLM11465 row: 1 column: 13  
High quality sequence stop: 805.

# FEATURES

Source  
1. .807  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5186388"  
/clone\_lib="NIH\_MGC\_116"  
/lab\_host="DH10B"  
/note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH\_MGC Library."

BASE COUNT 186 a 209 c 171 g 241 t  
ORIGIN  
Query Match 2.9%; Score 65; DB 13; Length 807;  
Best Local Similarity 100.0%; Pred. No. 5.3e-23;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 GTCATGCTGTGTGTTTAAAGCCAGGACGCTACCTTTGGGTGGTGACAAAGTGTG 525  
|||||  
Db 433 GTCATGCTGTGTGTTTAAAGCCAGGACGCTACCTTTGGGTGGTGACAAAGTGTG 492  
QY 526 ATCAC 530  
|||||  
Db 493 ATCAC 497

Search completed: June 1, 2003, 22:46:29  
Job time : 2856 secs

